

Amendments to the Specification:

On page 41, please replace the paragraph beginning on line 7 with the following:

The intention is to ascertain the optimal DNA sequence **(SEQ ID NO: 9)** pertaining to the (fictional) amino acid sequence AASeq1 **(SEQ ID NO:10)** from below. A conventional back-translation with optimization for optimal codon usage serves as reference.

On page 43, please replace the paragraphs beginning on line 11 and ending on line 35 with the following:

An optimization only for optimal codon usage results in the following sequence:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<u>SEQ ID NO: 10</u>	E	Q	F	I	I	K	N	M	F	I	I	K	N	A
<u>SEQ ID NO: 9</u>	GAA	CAG	TTT	ATT	ATT	AAA	AAC	ATG	TTT	ATT	ATT	AAA	AAC	GCG

It is characterized by the following properties:

- highly repetitive, caused by the amino acid sequence F_I_I_K_N (**residues 3-7 and 9-13 of SEQ ID NO: 10**) which appears twice (the repetitive sequence **(bases 7-21 and 25-39 of SEQ ID NO:9)** with the highest score (18) is shown):

19	AACATGTTTATTATTAAAAAC

2	AACA-GTTTATTATTAAAAAC

- GC content: 21.4%
- the Nla III recognition sequence CATG is present
- average codon usage 100

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If the optimization is carried out according to the algorithm of the invention with the abovementioned assessment functions and parameters, the following DNA sequence is obtained:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<u>SEQ ID NO: 10</u>	E__	Q__	F__	I__	I__	K__	N__	M__	F__	I__	I__	K__	N__	A__
<u>SEQ ID NO: 9</u>	GAA	CAG	TTC	ATC	ATC	AAA	AAT	ATG	TTT	ATT	ATC	AAG	AAC	GCG

On page 45, please replace the paragraph beginning on line 24 with the following:

The CDS are in this case arranged according to decreasing total score, i.e. the first codon of the first CDS shown is attached to the previously optimized DNA sequence. **The CDS in the following table correspond to sequences in the attached Sequence Listing, as shown below:**

<u>Starting</u> <u>Amino Acid</u>	<u>CDS</u>	<u>Test Sequence</u>
<u>1 E</u>	<u>SEQ ID NO: 11</u>	<u>bases 1-9 of SEQ ID NO: 9</u>
<u>2 Q</u>	<u>SEQ ID NO: 12</u>	<u>bases 1-12 of SEQ ID NO: 9</u>
<u>3 F</u>	<u>SEQ ID NO: 13</u>	<u>bases 1-15 of SEQ ID NO: 9</u>
<u>4 I</u>	<u>SEQ ID NO: 14</u>	<u>bases 1-18 of SEQ ID NO: 9</u>
<u>5 I</u>	<u>SEQ ID NO: 15</u>	<u>bases 1-21 of SEQ ID NO: 9</u>
<u>6 K</u>	<u>SEQ ID NO: 16</u>	<u>bases 1-24 of SEQ ID NO: 9</u>
<u>7 N</u>	<u>SEQ ID NO: 17</u>	<u>bases 1-27 of SEQ ID NO: 9</u>
<u>8 M</u>	<u>SEQ ID NO: 18</u>	<u>bases 1-30 of SEQ ID NO: 9</u>
<u>9 F</u>	<u>SEQ ID NO: 19</u>	<u>bases 1-33 of SEQ ID NO: 9</u>
<u>10 I</u>	<u>SEQ ID NO: 20</u>	<u>bases 1-36 of SEQ ID NO: 9</u>
<u>11 I</u>	<u>SEQ ID NO: 21</u>	<u>bases 1-39 of SEQ ID NO: 9</u>
<u>12 K</u>	<u>SEQ ID NO: 22</u>	<u>bases 1-42 of SEQ ID NO: 9</u>

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On page 53, please replace the paragraph beginning on line 6 with the following:

Origin of the amino acid sequence **(SEQ ID NO: 23):**

DEFINITION Aequorea victoria green-fluorescent protein mRNA, complete cds.

ACCESSION M62654

MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLLKFICTTGKLPVPWPTLVTTFSYGVQCFSRYPDHMKQHDFFKSAPEGYVQERTIFYKDDGNYKSRAEVKFEGLTLVNRIELKGIDFKEDGNILGHKMEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVT AAGITHGMDELYK

On page 58, please add the following paragraph after the table at line 12:

The following sequences in the tables above correspond to sequences in the attached Sequence Listing: Eukaria: (consensus) Spice Acceptor (SEQ ID NO: 24); Eukaria: RNA inhib. Sequence (SEQ ID NO: 25); Prokaria: RBS-Entry (2) (SEQ ID NO: 26); Prokaria: RBS-Entry (1) (SEQ ID NO: 27); Prokaria: RBS-Entry (3) (SEQ ID NO: 28); Prokaria: RBS-Entry (4) (SEQ ID NO: 29); Prokaria: RBS-Entry (5) (SEQ ID NO: 30); Prokaria: RBS-Entry (6) (SEQ ID NO: 31); Prokaria: RBS-Entry (7) (SEQ ID NO: 32).

On page 65, please replace the heading at lines 1-3 with the following:

Annex: SEQ-IDs and alignments of the DNA sequences used

The SEQ-ID references used herein correspond to the similarly-numbered sequences in the attached Sequence Listing, e.g., "SEQ-ID1" corresponds to SEQ ID NO: 1, "SEQ-ID2" corresponds to SEQ ID NO: 2, etc.

SEQ-ID of the indicated constructs:

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*Following the abstract, please replace the original Sequence Listing with the Substitute
Sequence Listing attached hereto as substitute sheets (10 pages).*